REMARKS

This document is submitsted in response to the Office Action mailed September 12, 2005 ("Office Action"). Claims 17-20, 22-24, 29, and 34-35 have been amended, and new claims 42-47 have been added. Claims 1-16 and 36-41 have been cancelled.

Support for the amendment to claim 17 is found in the Specification, e.g., at page 4, lines 27-28. Claim 18 has been amended to delete non-elected subject matter and to recite a proper antecedent basis in amended claim 17. Support for the amendment to claim 19 is found in the Specification at page 1, line 26 through page 2, line 15; page 3, lines 33-34; and page 4, lines 13-20. Claims 22 and 24 has been amended to correct the antecedent basis of a limitation. Claims 20, 23, and 29 has been amended to correct their dependencies. Claim 34 has been amended for clarity. Claim 35 has been amended to incorporate a limitation found in original claim 4 and is supported by the Specification, e.g., at page 3, lines 33-36 and page 4, lines 13-20. No new matter has been introduced.

Support for new claim 42, dependent from, claim 17 can be found in the Specification, e.g., at page 3, lines 12-21. Support for new claim 43, dependent from claim 34, can be found in the Specification, e.g., at page 1, lines 23-25; and page 3, line 35 through page 4, line 2. Support for new claim 44, dependent from claim 34, can be found in the Specification, e.g., at page 3, lines 12-21; and page 3, line 35 through page 4, line 2. Support for new independent claim 45, and claims 46-47 dependent from it, can be found in the Specification, e.g., at page 3, lines 12-21; and page 6, line 25 through page 7, line 7.

Upon entry of the proposed amendments, claims 17-20, 22-35, and 42-47 will be under examination. Reconsideration of the application is respectfully requested in view of the remarks below.

Objection to the Specification

The Office Action notes that the Specification contains an embedded hyperlink that must be deleted. See the Office Action, page 2, lines 10-12. The Specification has been so amended.

Claim Objections

Claims 17-20 and 22-35 were objected to for being drawn to non-elected inventions, and claims 19-20 and 23, 29-33, and 35 were objected to for being dependent on a non-elected claim. See the Office Action page 2, lines 14-17. The claims at issue have all been amended to recite the elected invention and species.

Claims 20, 23, and 29-33 were objected to under 37 C.F.R. § 1.75(c) as being in improper form, on the ground that a multiple dependent claim cannot depend from another multiple dependent claim. See page 3, lines 1-3. Applicant has amended these claims to correct the improper form of their dependencies.

The Office Action objects to dependent claims 19, 23, 24, 29, and 35 for improperly reciting the indefinite article "a" rather than the definite article "the" when referring to a limitation recited in a claim from which they depend. See page 3, lines 4-9. As amended, claims 19, 23, 24, 29, and 35 recite the definite article where appropriate.

In view of the amendments noted above, withdrawal of the objections is respectfully requested.

Rejections under 35 U.S.C. § 112, first paragraph (written description)

Claims 17-19, 22, 24-28, and 34 were rejected as failing to meet the written description requirement. See the Office Action, page 3, lines 17-20.

Claim 17 is drawn to nucleic acids that hybridize under high stringency to SEQ ID NO: 1 or a complementary sequence thereof. The Office Action concludes that Applicant fails to describe a representative number of polynucleotide sequences (i.e., "species") sufficient to demonstrate her possession of the claimed genus, as she teaches only one such sequence, i.e., SEQ ID NO: 1 itself. See page 5, lines 15-18. Applicant respectfully disagrees.

As amended, claim 17 covers a genus of nucleic acids containing a sequence of at least 500 bases that hybridizes under stringent conditions to SEQ ID NO: 1 or the complementary sequence thereof. It is submitsted that this claim is in line with United States Patent and Trademark Office policy regarding the written description requirement as set forth in the Revised Interim Written Description Guidelines published January 5, 2001, particularly the accompanying Training Materials ("Training Materials"). Amended claim 17 is analogous to the

claim presented in Example 9 of the Training Materials, which the Office deems to meet the written description requirement. The Example 9 claim is directed to a nucleic acid that hybridizes under stringent conditions to the complement of the disclosed reference sequence, wherein the sequence encodes a protein with specific functional properties.[1]

The Example 9 specification discloses a single sequence that falls within the genus covered by the claim. Example 9 concludes:

> [A] person of [ordinary] skill in the art would not expect substantial variation among species encompassed within the scope of the claim because the highly stringent hybridization conditions set forth in the claim yield structurally similar DNAs. Thus, a representative number of species is disclosed, since highly stringent hybridization conditions in combination with the coding function of DNA and the level of skill and knowledge in the art are adequate to determine that Applicant was in possession of the claimed invention. See Training Materials, page 36, lines 18-23; and page 37 lines 1-2.

By analogy, one of ordinary skill in the art would not expect substantial variation among the species encompassed by the genus of claim 17, as the stringent hybridization conditions recited will yield structurally similar DNA sequences. Of note, the "stringent" hybridization conditions recited by claim 17 and taught in the instant Specification, i.e., 0.5X SSC and 65 °C (page 5, lines 14-15) are even more so than those defined in Example 9, i.e., 6X SSC and 65 °C (page 35, lines 14-16). Thus, the genus of hybridizing nucleic acids covered by claim 17 is, if anything, even narrower than that of the Example 9 claim. Indeed, since the claimed genus is narrow, one species (i.e., SEQ ID NO: 1) is representative of the genus and therefore sufficient to demonstrate its possession, as in Example 9.

Based on the foregoing remarks, Applicant submits that claim 17 meets the written description requirement. For at least the same reasons, claims 18-19, 22, and 24-28, all of which depend from claim 17, and independent claim 34 also meet this requirement.

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[1] Applicant would like to point out that although SEQ ID NO: 1 encodes a protein with specific functional properties (i.e., binding to DNA containing one or more copies of a TATCCA sequence), claim 17 covers a genus of nucleic acids that merely hybridize to SEQ ID NO: 1 under stringent hybridization conditions. In other words, not all of the hybridizing nucleic acids within the genus encompassed by claim 17 will necessarily encode a protein, let alone a protein with specific functional properties.

Rejections under 35 U.S.C. § 112, first paragraph (enablement)

Claims 17-19, 22, 24-28, and 34 were rejected as lacking enablement. See the Office Action, page 6, lines 3-5.

With relevance to claim 17, the Office Action notes that "Applicant['s] claims are drawn to nucleic acid sequences that hybridize under stringent conditions to SEQ ID NO: 1, but the state-of-the-art teaches [that] isolating DNA fragments using stringent hybridization conditions does not always select for DNA fragments whose contiguous nucleotide sequence is the same or nearly the same as the probe." See page 8, line 21 through page 9, line 11. In support of this assertion, it refers to Fourgoux-Nicol *et al.* ("Fourgoux"). In particular, this reference discloses that a 497 base pair (bp) probe was successfully used to isolate a 674 bp DNA fragment under high stringency conditions, despite the fact that the longest contiguous stretch of sequence to which the probe could hybridize consisted of 93 bps. See page 9, lines 2-11.

Applicant does not dispute the Office Action's contention that high stringency hybridization may yield nucleic acid fragments of limited identity to a reference sequence. Nevertheless, insofar as such fragments meet the length and stringent hybridization requirements recited in amended claim 17, they fall within the covered genus.[2] In any event, Applicant would like to point out that at the time of filing, the art recognized an *a priori* quantifiable relationship between probe-target melting temperature (Tm) and probe-target duplex length, GC content, and number of mismatches vis-à-vis hybridization conditions. Tm increases with increasing probe-target duplex length and GC content, and decreases for every probe-target mismatch. Formulas for predicting the Tm of a probe-target duplex, based on these relationships, were known long before the time of filing. See, e.g, Sambrook *et al.* (1989), *Molecular Cloning: A Laboratory Manual* (2nd ed.), page 9.51. Applicant therefore submits that given the hybridizing sequence length requirements and stringent hybridization conditions recited in claim 17, the covered genus is predictably quite narrow, even allowing for DNA fragments that have a relatively short stretch of contiguous hybridizing sequence such as the one disclosed in Fourgoux.

[2] Of note, such fragments can be used, e.g., to detect a nucleic acid containing the SEQ ID NO: 1 sequence, e.g., a rice plant mRNA in containing the SEQ ID NO: 1 sequence. See, e.g., the Specification at page 4, line 30 through page 5, line 2.

The Office Action further states that "[Applicant has not] disclosed how one makes or isolates any of the sequences that are encompassed by [Applicant's] broad claims. [Applicant has not taught] which regions of the respective polynucleotides can be used to amplify any of said polynucleotides or which regions can be used as a probe to isolate any of said polynucleotide sequences." See page 10, lines 3-7. Applicant disagrees.

Indeed, the Office Action itself acknowledges that Applicant discloses a hybridization probe, consisting of 660 BPS of SEQ ID NO: 1. See page 7, lines 15-19. Further, the Specification teaches primers for amplifying a SEQ ID NO: 1 subsequence, i.e., a nucleic acid that clearly falls within the genus encompassed by claim 17. See page 13, lines 18-22. In other words, the Specification does teach regions of the reference sequence that can be used as probes to identify or amplify sequences of the genus covered by claim 17, contrary to the Office Action's assertions above. In addition, the design of hybridization probes and primers, based on a known sequence (e.g., SEQ ID NO: 1), was quite routine in the art at the time of filing, as was their use for isolating nucleic acids containing related, hybridizing sequences. See, e.g., Sambrook *et al.* (2001) *Molecular Cloning: A Laboratory Manual* (3rd ed.), chapters 8-11. It follows that one of ordinary skill in the art would not face an undue burden in isolating the predictably limited number of nucleic acids containing sequences that meet the length and hybridization requirements set forth in amended claim 17. Applicant therefore submits that this claim is enabled. For at least the same reasons, claims 18-19, 22, and 24-28, dependent from claim 17, and claim 34 also meet this requirement.

For the foregoing reasons, claims 17-19, 22, 24-28, and 34 meet both the written description requirement and the enablement requirement. Withdrawal of the rejections is respectfully requested.

Rejections under 35 U.S.C. § 102(a)

Claims 17 and 18 were rejected as being anticipated by Dong *et al.* ("Dong"). See the Office Action, page 10, lines 18-21.

In particular, the Office Action notes that Dong discloses a nucleic acid containing 92% identity to nucleotides 993-1324 of SEQ ID NO: 1. On this basis, it concludes that the Dong nucleic acid would hybridize to SEQ ID NO: 1 or a complement thereof under stringent

hybridization conditions, as required by claim 17. See page 11, lines 6-9. Of note, the Office interprets hybridization to "a complementary sequence" of SEQ ID NO: 1 to "read on as little as one hybridizing bp." See page 11, lines 4-5.

Applicant notes that claim 17, as amended, requires a nucleic acid containing a hybridizing sequence of at least 500 bases that hybridizes to SEQ ID NO: 1 or the complement thereof. As the Dong sequence hybridizes to SEQ ID NO: 1 over nucleotides 993-1324, i.e., a length of 332 bases, the Dong hybridizing sequence fails to meet the hybridizing length requirement recited in the amended claim. Importantly, as amended claim 17 recites "the complementary sequence thereof," it is clear, based on the meaning of this phrase in the art, that it refers to a full length complementary sequence of SEQ ID NO: 1, rather than a complementary sequence of any length. Thus, it is submitsted claim 17 is not anticipated by Dong. For at least the same reasons, neither is claim 18 dependent from it.

Rejections under 35 U.S.C. § 102(b)

Claims 17-18, 22, and 24 were rejected as being anticipated by Klessig *et al.* ("Klessig"). See the Office Action, page 11, lines 10-14. Specifically, the Office Action refers to a nucleic acid sequence disclosed in Klessig ("Klessig Sequence") that encodes a myb protein. It concludes that the Klessig Sequence anticipates claim 17 on this basis and in view of its interpretation of "a complementary sequence thereof," as discussed above. See page 11, line 15 through page 12, line 2. Applicant respectfully disagrees.

A sequence alignment of the Klessig Sequence to SEQ ID NO: 1, attached hereto as "Exhibit A," reveals no significant identity between these two sequences. Consequently, the Klessig Sequence would certainly not be expected to hybridize to SEQ ID NO: 1 under stringent conditions, as required by claim 17. Moreover, as amended claim 17 recites "the complementary sequence thereof" rather than "a complementary sequence thereof," the Klessig Sequence, for this reason as well, clearly does not meet the sequence hybridization requirements set forth in amended claim 17. It is therefore submitsted that this claim is not anticipated by Klessig, and that for at least the same reasons, claims 18, 22, and 24, dependent from claim 17, are also not anticipated by this reference.

New Claims

It is submitted that new claims 42-47 are allowable for at least the reasons set forth above.

CONCLUSION

Applicant submits that the grounds for the rejections asserted in the Office Action have been overcome, and that the claims, as pending, define subject matter that meets the written description, enablement, and novelty requirements. It is further submitsted that the new claims cover allowable subject matter. Thus, allowance of this application is proper, and early favorable action is respectfully solicited

Enclosed is a $60 check for the Petition for Extension of Time fee. Please apply any other charges or credits to deposit account 06-1050 referencing attorney docket 08919-088001.

Respectfully submitsted,

Date: 1-12-06

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Alignment of Sequence (SEQ ID NO:1) from Klessig *et al.* U.S. Patent No. 5,939,601 "Klessig"
vs
SEQ ID NO:1

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.12 [Aug-07-2005]

Match: 1 Mismatch: -2 gap open: 0 gap extension: 0
x_dropoff: 50 expect: 50.00 wordsize: 28 Filter Align

Sequence 1 lcl|seq_1 **Length** 1344 (Klessig)
K
Sequence 2 lcl|seq_2 **Length** 1330 (SEQ ID NO:1)

No significant similarity was found

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CPU time:      0.01 user secs.      0.02 sys. secs          0.03 total secs.

Lambda      K       H
    1.33     0.621      1.12

Gapped
Lambda      K       H
    1.28     0.460     0.850


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 1
Number of Hits to DB: 0
Number of sequences better than 50.0: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 1344
Length of database: 16,404,110,021
Length adjustment: 33
Effective length of query: 1311
Effective length of database: 16,404,109,988
Effective search space: 21505788194268
Effective search space used: 21505788194268
X1: 11 (21.1 bits)
X2: 27 (49.9 bits)
X3: 27 (49.9 bits)
S1: 13 (25.7 bits)
S2: 21 (39.9 bits)
```

Klessig Sequence:

1 CTTTTTGGCA TTTCTTTCGT CCTTTTGGGA AGAAAGAAA G AGTGAAAGAA 51 ATACCTAAAA
CCAAGGAGAA TTCAGAAAGA TAGCCGAAG A AGAAAAAAAA 101 ACAAGTGATC AATTTTTCAA
GAGGAAGAAG AGATCAAGC A AAAGAAAATG 151 GTGAGAGCTC CTTGTTGTGA GAAAATGGGG
CTGAAAAAA G GGCCATGGAT 201 TCCTGAAGAA GATCAGATTC TCATCTCTTT CATTCAAAC T
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AGTTGCAGAC TGCGGTGGAC GAATTATTTG CGACCAGAT A TAAAGAGGGG 351 AAATTTCACC
AAGGAAGAAG AAGAAACAAT TATCCAGTT A CATGAAATGC 401 TTGGCAATAG ATGGTCTGCA
ATAGCAGCAA AATTACCAG G ACGAACAGAC 451 AATGAAATAA AAAATGTTTG GCACACCCAC
TTGAAGAAG A AGCTCAAAGA 501 TTATAAGCCT CCTCAGAACT CCAAAAGACA CTCCAAGTC C
AAGAATCATG 551 ATTCCAAGGG TCCTACTACT TCTGAATCAT CCAATAATT C TGATCTTACT 601
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TCATCTAGTA CTGAAATGTC AACTGTGAC A CTAGTCGATG 701 ATCATCAAAT GGTTGTGATT
AAGCAAGAAG TAATGGAGT C GTCCGAGTAT 751 TTTCCAGAGA TCGATGAGAG TTTTTGGACG
GACGAATTA A CAACGGACAA 801 TAACTGGAGT AGTACTGATC ATGTTATGGT TGCTGCTAA T
CAAGAATTAC 851 AAGTTCAATT ACCATTTTCC AGTTTTAAGG AAGAAAATG T GGACATTTTG 901
GCTACAAAAA TGGAGGATGA CATGGACTTT TGGTACAAT G TTTTCATAAA 951 GACTGATGAT
TTGCCAGAAT TACCAGAATT TTGAGGGGG C TATGTTATAA 1001 TTTTGGTTCT TCTGTAAATT
TTGAGGTAGT GGTATCTAG C TAATAAATAG 1051 GTTGTAGAGA ATTTTTGGAG TCGGTAAGTT
TGAAACTTC G TGTTTGTAAT 1101 TTTCTTGACC AGAAAAATTT CCCGTGTTGG GACCATTAG C
TAGTATATTT 1151 TTGGTGTTAG TTATTTTGAA CCCTTCTTAC TTAGTTTTA G TGGGAGAAGT 1201
GTAAGTGGAT ATGCTGATGT GTTTTGTATT GACTTAGGA A TGTAGTTCCA 1251 TATATAGGCA
CAGAAAATCT ATATTTAGAG AAAAATTAT C GGAAAACCTA 1301 TAGTCACCAT CCTCCTAACT
TAACTTAAAA AAAAAAAAA A AAAA

SEQ ID NO:1

GTGCGAGATCCACCACCCGATGACCTCCCAGGCGGCGACGACGACGACCACGGCGGCGGCGGCGGCG
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